

0590
2/15

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OIPE

RAW SEQUENCE LISTING

DATE: 02/14/2002

PATENT APPLICATION: US/10/054,579

TIME: 16:11:10

Input Set : A:\LEX-0300-USA SEQLIST.txt

Output Set: N:\CRF3\02142002\J054579.raw

ENTERED

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4 <110> APPLICANT: Turner, C. Alexander Jr.
5      Mathur, Brian
7 <120> TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
9 <130> FILE REFERENCE: LEX-0300-USA
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/054,579
C--> 11 <141> CURRENT FILING DATE: 2002-01-22
11 <150> PRIOR APPLICATION NUMBER: US 60/263,378
12 <151> PRIOR FILING DATE: 2001-01-23
14 <160> NUMBER OF SEQ ID NOS: 4
16 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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19 <211> LENGTH: 2007
20 <212> TYPE: DNA
21 <213> ORGANISM: homo sapiens
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25 ctggagaaga cgctgggcaa ggggcagaca ggtctggtga agctgggggt tactgctgc 120
26 acctgccaga aggtggccat caagatcgtc aacctgaga agctcagcga gtcggtgctg 180
27 atgaaggtgg agcgggagat cgcgacctg aagctcattg agcaccacca cgtcctaaag 240
28 ctgcacgacg tttatgaaaa caaaaaatat ttgtacctgg tgctagaaca cgtgtcaggt 300
29 ggtgagctct tcgactacct ggtgaagaag gggaggctga cgcctaagga ggctcggaag 360
30 ttcttcctggc agatcatctc tgcgctggac ttctgccaca gccactccat atgccacagg 420
31 gatctgaaac ctgaaaacct cctgctggac gagaagaaca acatccgcat cgcagacttt 480
32 ggcattggcgt ccctgcaggt tggcgacagc ctgttggaga ccagctgtgg gtccccccac 540
33 tacgctgccc ccgaggtgat ccggggggag aagtatgacg gccggaaggc ggacgtgtgg 600
34 agctgcggcg tcatcctgtt cgccttgctg gtcggggctc tgcccttcga cgatgacaac 660
35 ttgcgcagagc tgctggagaa ggtgaagcgg gtcgtgttcc acatgccgca ctttatcccg 720
36 cccgactgcc agagtctgct acggggcatg atcgaggtgg acgccgcacg ccgcctcacg 780
37 ctgagagcaca ttcagaaaca catatggtat atagggggca agaattgagcc cgaaccagag 840
38 cagcccattc ctgcgaaggt gcagatccgc tcgctgcccc gcctggagga catcgacccc 900
39 gacgtgctgg acagcatgca ctactgggc tgcttccgag accgcaacaa gctgctgcag 960
40 gacctgctgt ccgaggagga gaaccaggag aagatgattt acttcctcct cctggaccgg 1020
41 aaagaaaggt acccgagcca ggaggatgag gacctgcccc cccggaacga gatagaccct 1080
42 ccccggaagc gtgtggactc cccgatgctg aaccggcacg gcaagcggcg gccagaacgc 1140
43 aaatccatgg aggtgctcag cgtgacggac ggcggctccc cggtgctgc gcggcgggcc 1200
44 attgagatgg cccagcacgg ccagaggtct cgggtccatca gcggtgcctc ctcaaggcctt 1260
45 tccaccagcc cactcagcag ccccggggtg acccctcacc cctcaccaag gggcagtccc 1320
46 ctccccaccc ccaaggggac acctgtccac acgccaagg agagcccggc tggcacgccc 1380
47 aacccccacg ccccgctccag ccccgcgctc ggaggggtgc cctggagggg gcggctcaac 1440
48 tccatcaaga acagctttct gggtcacccc cgcttccacc gccggaaact gcaagttccg 1500
49 acgccggagg agatgtccaa cctgacacca gagtcgtccc cagagctggc gaagaagtcc 1560
50 tggtttggga acttcatcag cctggagaag gaggagcaga tcttcgtggt catcaaagac 1620
51 aaacctctga gctccatcaa ggctgacatc gtgcacgcct tctgtcgtat tcccagtctc 1680

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52 agccacagcg tcattctccca aacgagcttc cggggccgagt acaaggccac ggggggggcca 1740
53 gccgtgttcc agaagccggt caagttccag gttgatata cctacacgga ggggtggggag 1800
54 gcgcagaagg agaacggcat ctactccgtc accttcaccc tgctctcagg cccagccgt 1860
55 cgcttcaaga ggggtgggtga gaccatccag gccagctgc tgagcacaca cgaccgcct 1920
56 gcggcccagc acttgtcaga caccactaac tgtatggaaa tgatgacggg gcggctttcc 1980
57 aaatgtgga ttatcccgaa aagttaa 2007
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60 <211> LENGTH: 668
61 <212> TYPE: PRT
62 <213> ORGANISM: homo sapiens
64 <400> SEQUENCE: 2
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66 1 5 10 15
67 Gly Pro Tyr Arg Leu Glu Lys Thr Leu Gly Lys Gly Gln Thr Gly Leu
68 20 25 30
69 Val Lys Leu Gly Val His Cys Val Thr Cys Gln Lys Val Ala Ile Lys
70 35 40 45
71 Ile Val Asn Arg Glu Lys Leu Ser Glu Ser Val Leu Met Lys Val Glu
72 50 55 60
73 Arg Glu Ile Ala Ile Leu Lys Leu Ile Glu His Pro His Val Leu Lys
74 65 70 75 80
75 Leu His Asp Val Tyr Glu Asn Lys Lys Tyr Leu Tyr Leu Val Leu Glu
76 85 90 95
77 His Val Ser Gly Gly Glu Leu Phe Asp Tyr Leu Val Lys Lys Gly Arg
78 100 105 110
79 Leu Thr Pro Lys Glu Ala Arg Lys Phe Phe Arg Gln Ile Ile Ser Ala
80 115 120 125
81 Leu Asp Phe Cys His Ser His Ser Ile Cys His Arg Asp Leu Lys Pro
82 130 135 140
83 Glu Asn Leu Leu Leu Asp Glu Lys Asn Asn Ile Arg Ile Ala Asp Phe
84 145 150 155 160
85 Gly Met Ala Ser Leu Gln Val Gly Asp Ser Leu Leu Glu Thr Ser Cys
86 165 170 175
87 Gly Ser Pro His Tyr Ala Cys Pro Glu Val Ile Arg Gly Glu Lys Tyr
88 180 185 190
89 Asp Gly Arg Lys Ala Asp Val Trp Ser Cys Gly Val Ile Leu Phe Ala
90 195 200 205
91 Leu Leu Val Gly Ala Leu Pro Phe Asp Asp Asp Asn Leu Arg Gln Leu
92 210 215 220
93 Leu Glu Lys Val Lys Arg Gly Val Phe His Met Pro His Phe Ile Pro
94 225 230 235 240
95 Pro Asp Cys Gln Ser Leu Leu Arg Gly Met Ile Glu Val Asp Ala Ala
96 245 250 255
97 Arg Arg Leu Thr Leu Glu His Ile Gln Lys His Ile Trp Tyr Ile Gly
98 260 265 270
99 Gly Lys Asn Glu Pro Glu Pro Glu Gln Pro Ile Pro Arg Lys Val Gln
100 275 280 285
101 Ile Arg Ser Leu Pro Ser Leu Glu Asp Ile Asp Pro Asp Val Leu Asp
102 290 295 300

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103 Ser Met His Ser Leu Gly Cys Phe Arg Asp Arg Asn Lys Leu Leu Gln
104 305 310 315 320
105 Asp Leu Leu Ser Glu Glu Glu Asn Gln Glu Lys Met Ile Tyr Phe Leu
106 325 330 335
107 Leu Leu Asp Arg Lys Glu Arg Tyr Pro Ser Gln Glu Asp Glu Asp Leu
108 340 345 350
109 Pro Pro Arg Asn Glu Ile Asp Pro Pro Arg Lys Arg Val Asp Ser Pro
110 355 360 365
111 Met Leu Asn Arg His Gly Lys Arg Arg Pro Glu Arg Lys Ser Met Glu
112 370 375 380
113 Val Leu Ser Val Thr Asp Gly Gly Ser Pro Val Pro Ala Arg Arg Ala
114 385 390 395 400
115 Ile Glu Met Ala Gln His Gly Gln Arg Ser Arg Ser Ile Ser Gly Ala
116 405 410 415
117 Ser Ser Gly Leu Ser Thr Ser Pro Leu Ser Ser Pro Arg Val Thr Pro
118 420 425 430
119 His Pro Ser Pro Arg Gly Ser Pro Leu Pro Thr Pro Lys Gly Thr Pro
120 435 440 445
121 Val His Thr Pro Lys Glu Ser Pro Ala Gly Thr Pro Asn Pro Thr Pro
122 450 455 460
123 Pro Ser Ser Pro Ser Val Gly Gly Val Pro Trp Arg Ala Arg Leu Asn
124 465 470 475 480
125 Ser Ile Lys Asn Ser Phe Leu Gly Ser Pro Arg Phe His Arg Arg Lys
126 485 490 495
127 Leu Gln Val Pro Thr Pro Glu Glu Met Ser Asn Leu Thr Pro Glu Ser
128 500 505 510
129 Ser Pro Glu Leu Ala Lys Lys Ser Trp Phe Gly Asn Phe Ile Ser Leu
130 515 520 525
131 Glu Lys Glu Glu Gln Ile Phe Val Val Ile Lys Asp Lys Pro Leu Ser
132 530 535 540
133 Ser Ile Lys Ala Asp Ile Val His Ala Phe Leu Ser Ile Pro Ser Leu
134 545 550 555 560
135 Ser His Ser Val Ile Ser Gln Thr Ser Phe Arg Ala Glu Tyr Lys Ala
136 565 570 575
137 Thr Gly Gly Pro Ala Val Phe Gln Lys Pro Val Lys Phe Gln Val Asp
138 580 585 590
139 Ile Thr Tyr Thr Glu Gly Gly Glu Ala Gln Lys Glu Asn Gly Ile Tyr
140 595 600 605
141 Ser Val Thr Phe Thr Leu Leu Ser Gly Pro Ser Arg Arg Phe Lys Arg
142 610 615 620
143 Val Val Glu Thr Ile Gln Ala Gln Leu Leu Ser Thr His Asp Pro Pro
144 625 630 635 640
145 Ala Ala Gln His Leu Ser Asp Thr Thr Asn Cys Met Glu Met Met Thr
146 645 650 655
147 Gly Arg Leu Ser Lys Cys Gly Ile Ile Pro Lys Ser
148 660 665
151 <210> SEQ ID NO: 3
152 <211> LENGTH: 1827
153 <212> TYPE: DNA

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154 <213> ORGANISM: homo sapiens
156 <400> SEQUENCE: 3
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158 ctgcacgacg tttatgaaaa caaaaaatat ttgtacctgg tgctagaaca cgtgtcaggt 120
159 ggtgagctct tcgactacct ggtgaagaag gggaggctga cgcctaagga ggctcgggaag 180
160 ttcttccggc agatcatctc tgcgctggac ttctgccaca gccactccat atgccacagg 240
161 gatctgaaac ctgaaaacct cctgctggac gagaagaaca acatccgcat cgcagacttt 300
162 ggcattggcg cctgcagggt tggcgacagc ctggttgaga ccagctgtgg gtccccccac 360
163 tacgcctgcc ccgaggatgat ccggggggag aagtatgacg gccggaaggc ggacgtgtgg 420
164 agctgcggcg tcactctgtt cgccttgctg gtgggggctc tgcccttcga cgatgacaac 480
165 ttgcgacagc tgctggagaa ggtgaagcgg ggcgtgttcc acatgccgca ctttatcccg 540
166 cccgactgcc agagtctgct acggggcatg atcgagggtg acgccgcacg ccgcctcacg 600
167 ctagagcaca ttcagaaaca catatggtat atagggggca agaattagcc cgaaccagag 660
168 cagcccattc ctgcgaaggt gcagatccgc tcgctgcccc gccctggagg catcgacccc 720
169 gacgtgctgg acagcatgca ctactgggc tgcttccgag accgcaacaa gctgctgcag 780
170 gacctgctgt ccgaggagga gaaccaggag aagatgattt acttctctct cctggaccgg 840
171 aaagaaaggt acccgagcca ggaggatgag gacctgcccc cccggaacga gatagacct 900
172 ccccggaagc gtgtggactc cccgatgctg aaccggcacg gcaagcggcg gccagaacgc 960
173 aaatccatgg aggtgctcag cgtgacggac ggcggctccc cggtgctgc gcggcggggc 1020
174 attgagatgg ccagcacgag ccagagggtc cggctccatc gcggtgcctc ctcaggcctt 1080
175 tccaccagcc cactcagcag ccccggggtg acccctcacc cctcaccaag gggcagtcct 1140
176 ctccccaccc ccaaggggac acctgtccac acgccaaagg agagcccggc tggcacgccc 1200
177 aacccacgc ccccgctccag ccccgagctc ggaggggtgc cctggagggc gcggctcaac 1260
178 tccatcaaga acagctttct gggctcacc cgttccacc gccggaact gcaagttccg 1320
179 acgccggagg agatgtccaa cctgacacca gagtcgtccc cagagctggc gaagaagtcc 1380
180 tggtttgga acttcatcag cctggagaag gaggagcaga tcttcgtggt catcaaagac 1440
181 aaacctctga gctccatcaa ggctgacatc gtgcacgcct tcctgtcgat tcccagcttc 1500
182 agccacagcg tcacttccca aacgagcttc cgggcccagt acaaggccac gggggggcca 1560
183 gccgtgttcc agaagccggc caagttccag gttgatatca cctacacgga ggggtggggag 1620
184 gcgcagaagg agaacggcat ctactccgtc accttcccc tgctctcagg cccagccgt 1680
185 cgcttcaaga ggggtgtgga gaccatccag gccagctgc tgagcacaca cgaccgcct 1740
186 gcggccagc acttgcaga caccactaac tgtatggaaa tgatgacggg gcggctttcc 1800
187 aaatgtgga ttatccgaa aagttaa 1827
189 <210> SEQ ID NO: 4
190 <211> LENGTH: 608
191 <212> TYPE: PRT
192 <213> ORGANISM: homo sapiens
194 <400> SEQUENCE: 4
195 Met Lys Val Glu Arg Glu Ile Ala Ile Leu Lys Leu Ile Glu His Pro
196 1 5 10 15
197 His Val Leu Lys Leu His Asp Val Tyr Glu Asn Lys Lys Tyr Leu Tyr
198 20 25 30
199 Leu Val Leu Glu His Val Ser Gly Gly Glu Leu Phe Asp Tyr Leu Val
200 35 40 45
201 Lys Lys Gly Arg Leu Thr Pro Lys Glu Ala Arg Lys Phe Phe Arg Gln
202 50 55 60
203 Ile Ile Ser Ala Leu Asp Phe Cys His Ser His Ser Ile Cys His Arg
204 65 70 75 80
205 Asp Leu Lys Pro Glu Asn Leu Leu Leu Asp Glu Lys Asn Asn Ile Arg

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206				85				90				95				
207	Ile	Ala	Asp	Phe	Gly	Met	Ala	Ser	Leu	Gln	Val	Gly	Asp	Ser	Leu	Leu
208				100					105				110			
209	Glu	Thr	Ser	Cys	Gly	Ser	Pro	His	Tyr	Ala	Cys	Pro	Glu	Val	Ile	Arg
210				115				120					125			
211	Gly	Glu	Lys	Tyr	Asp	Gly	Arg	Lys	Ala	Asp	Val	Trp	Ser	Cys	Gly	Val
212		130					135					140				
213	Ile	Leu	Phe	Ala	Leu	Leu	Val	Gly	Ala	Leu	Pro	Phe	Asp	Asp	Asp	Asn
214	145					150					155				160	
215	Leu	Arg	Gln	Leu	Leu	Glu	Lys	Val	Lys	Arg	Gly	Val	Phe	His	Met	Pro
216				165					170					175		
217	His	Phe	Ile	Pro	Pro	Asp	Cys	Gln	Ser	Leu	Leu	Arg	Gly	Met	Ile	Glu
218				180					185				190			
219	Val	Asp	Ala	Ala	Arg	Arg	Leu	Thr	Leu	Glu	His	Ile	Gln	Lys	His	Ile
220			195					200					205			
221	Trp	Tyr	Ile	Gly	Gly	Lys	Asn	Glu	Pro	Glu	Pro	Glu	Gln	Pro	Ile	Pro
222		210					215					220				
223	Arg	Lys	Val	Gln	Ile	Arg	Ser	Leu	Pro	Ser	Leu	Glu	Asp	Ile	Asp	Pro
224	225					230					235				240	
225	Asp	Val	Leu	Asp	Ser	Met	His	Ser	Leu	Gly	Cys	Phe	Arg	Asp	Arg	Asn
226				245					250					255		
227	Lys	Leu	Leu	Gln	Asp	Leu	Leu	Ser	Glu	Glu	Glu	Asn	Gln	Glu	Lys	Met
228				260					265				270			
229	Ile	Tyr	Phe	Leu	Leu	Leu	Asp	Arg	Lys	Glu	Arg	Tyr	Pro	Ser	Gln	Glu
230			275					280					285			
231	Asp	Glu	Asp	Leu	Pro	Pro	Arg	Asn	Glu	Ile	Asp	Pro	Pro	Arg	Lys	Arg
232		290					295					300				
233	Val	Asp	Ser	Pro	Met	Leu	Asn	Arg	His	Gly	Lys	Arg	Arg	Pro	Glu	Arg
234	305					310					315				320	
235	Lys	Ser	Met	Glu	Val	Leu	Ser	Val	Thr	Asp	Gly	Gly	Ser	Pro	Val	Pro
236				325					330					335		
237	Ala	Arg	Arg	Ala	Ile	Glu	Met	Ala	Gln	His	Gly	Gln	Arg	Ser	Arg	Ser
238				340					345				350			
239	Ile	Ser	Gly	Ala	Ser	Ser	Gly	Leu	Ser	Thr	Ser	Pro	Leu	Ser	Ser	Pro
240			355					360					365			
241	Arg	Val	Thr	Pro	His	Pro	Ser	Pro	Arg	Gly	Ser	Pro	Leu	Pro	Thr	Pro
242		370				375						380				
243	Lys	Gly	Thr	Pro	Val	His	Thr	Pro	Lys	Glu	Ser	Pro	Ala	Gly	Thr	Pro
244	385					390				395					400	
245	Asn	Pro	Thr	Pro	Pro	Ser	Ser	Pro	Ser	Val	Gly	Gly	Val	Pro	Trp	Arg
246				405					410					415		
247	Ala	Arg	Leu	Asn	Ser	Ile	Lys	Asn	Ser	Phe	Leu	Gly	Ser	Pro	Arg	Phe
248				420					425				430			
249	His	Arg	Arg	Lys	Leu	Gln	Val	Pro	Thr	Pro	Glu	Glu	Met	Ser	Asn	Leu
250			435					440					445			
251	Thr	Pro	Glu	Ser	Ser	Pro	Glu	Leu	Ala	Lys	Lys	Ser	Trp	Phe	Gly	Asn
252		450				455						460				
253	Phe	Ile	Ser	Leu	Glu	Lys	Glu	Glu	Gln	Ile	Phe	Val	Val	Ile	Lys	Asp
254	465					470				475					480	

VERIFICATION SUMMARY

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Input Set : A:\LEX-0300-USA SEQLIST.txt

Output Set: N:\CRF3\02142002\J054579.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date